WHAT IS CLAIMED IS:

1. A method for identifying a subject at risk for the development of cancer comprising:

   (a) obtaining a test sample from a subject;

   (b) providing an RPL 14, CD39L3, PMGM, or GC20 gene probe;

   (c) contacting said probe with said test sample; and

   (d) analyzing DNA from said test sample,

   whereby aberrations in the hybridization of said probe to said DNA, as compared to wild-type DNA, indicates risk for the development of cancer.

2. The method of claim 1, wherein said test sample comprises a surgical or biopsy specimen, a paraffin embedded tissue, a frozen tissue imprint, a sputum, a lavages, a peripheral blood lymphocytes, a urinary specimen such as a bladder washing and urine, esophageal brush, a fine needle aspiration, a buccal smear or a bronchial lavage.

3. The method of claim 1, wherein said cancer is lung cancer.

4. The method of claim 1, wherein said cancer is an upper airway primary or secondary cancer.

5. The method of claim 1, wherein said cancer is bladder cancer.

6. The method of claim 1, wherein said cancer is cancer of the head or neck.

7. The method of claim 1, wherein said cancer is urothelial.

8. The method of claim 1, wherein said cancer is cancer of the kidneys.

9. The method of claim 1, wherein said cancer is cancer of the pancreas.

10. The method of claim 1, wherein said cancer is cancer of the mouth, throat, pharynx, larynx, or esophagus,

11. The method of claim 1, wherein said subject is a smoker.

12. The method of claim 1, wherein said subject is a former smoker.

13. The method of claim 1, wherein said subject is a non-smoker.

14. The method of claim 1, wherein said test sample comes from said subject who has not previously been diagnosed with cancer.

15. The method of claim 1, wherein said probe is labeled with a fluorophore.

16. The method of claim 1, wherein said probe is labeled with digoxigenin.

17. The method of claim 1, wherein said probe size is between 1000 and 2000 base pairs.

18. The method in claim 1, further comprising a spiral CT-scan.

19. The method of claim 1, further comprising administering to said subject chemopreventive drugs, nutritional supplements, chemotherapeutic drugs or biological modifying respdase drugs.

20. The method of claim 1, wherein said method is used to identify subjects who need an intensive follow-up protocol.

21. The probe of claim 1, wherein said probe is used to identify subjects who are suitable for novel investigational therapeutic approaches.

22. The method of claim 1, wherein a control probe is used.

23. The method of claim 22, wherein said control probe is labeled with a fluorophore.

24. The method of claim 23, wherein said control probe is labeled with spectrum orange.

25. The method of claim 22, wherein said control probe is a chromosome 3 stable marker.

26. The method of claim 25, wherein said control probe is Centromere 3 (CEP 3)

27. The method of claim 1, wherein analyzing comprises using FISH.

28. The probe of claim 1, wherein said probe is used as a biomarker for the early detection of early neoplastic events or cancer.

29. The method of claim 1, further comprising a 10q22 DNA probe.

30. A method for identifying a subject at risk for the development, recurrence, or metastasis of cancer comprising:

(a) obtaining a lung test sample from a subject;
(b) providing a 10q22 DNA probe;
(c) contacting said probe with said test sample; and
(d) analyzing DNA from said test sample,

whereby aberrations in the hybridization of said probe to said DNA, as compared to a centromeric DNA probe for chromosome 10, indicates the risk for the development, recurrence, or metastasis of cancer.

31. The method of claim 30, wherein said test sample comprises a surgical or biopsy specimen, a paraffin embedded tissue, a frozen tissue imprint, a sputum, a lavages, a peripheral blood lymphocytes, a urinary specimen such as a bladder washing and urine, esophageal brush, a fine needle aspiration, a buccal smear or a bronchial lavage.

32. The method of claim 30, wherein said cancer is lung cancer.

33. The method of claim 30, wherein said cancer is an upper airway primary or secondary cancer.

34. The method of claim 30, wherein said cancer is bladder cancer.

35. The method of claim 30, wherein said cancer is cancer of the head or neck.

36. The method of claim 30, wherein said cancer is urithial.

37. The method of claim 30, wherein said cancer is cancer of the kidneys.

38. The method of claim 30, wherein said cancer is cancer of the pancreas.

39. The method of claim 30, wherein said cancer is cancer of the mouth, throat, pharynx, larynx, or esophagus,

40. The method of claim 30, wherein said subject is a smoker.

41. The method of claim 30, wherein said subject is a non-smoker.

42. The method of claim 30, wherein said subject is a former smoker.

43. The method of claim 30, wherein said test sample comes from said subject who has not previously been diagnosed with cancer.

44. The method of claim 30, wherein said probe is labeled with a fluorophore.

45. The method of claim 30, wherein said probe is labeled with digoxigenin.

46. The method of claim 30, wherein said probe size is from 1000 to 2000 base pairs.

47. The method in claim 30, further comprising a spiral CT-scan.

48. The method of claim 30, wherein said method is used to identify subjects who need an intensive follow-up protocol.

49. The probe of claim 30, wherein said probe is used to identify subjects who are suitable for novel investigational therapeutic approaches.

50. The method of claim 30, wherein a control probe is used.

51. The method of claim 50, wherein said control probe is labeled with a fluorophore.

52. The method of claim 51 wherein said control probe is labeled with spectrum orange.

53. The method of claim 50, wherein said control probe is a chromosome 10 stable marker.

54. The method of claim 53, wherein said control probe is Centromere10 (CEP10).

55. The method of claim 30, wherein analyzing comprises using FISH.

56. The probe of claim 30, wherein said probe is used as a biomarker for the early detection of a tobacco related cancer.

57. A method for predicting the progression or metastasis of non-small cell carcinoma and other carcinoma in a subject comprising:

(a) obtaining a test sample from a subject;
(b) providing an RPL14, CD39L3, PMGM, or GC20 gene probe;
(c) contacting said probe with said test sample; and
(d) analyzing DNA from said test sample.

58. The method of claim 57, wherein said cancer is lung cancer.

59. The method of claim 57, wherein said cancer is an upper airway primary or secondary cancer.

60. The method of claim 57, wherein said cancer is bladder cancer.

61. The method of claim 57, wherein said cancer is cancer of the head or neck.

62. The method of claim 57, wherein said cancer is urithial.

63. The method of claim 57, wherein said cancer is cancer of the kidneys.

64. The method of claim 57, wherein said cancer is cancer of the pancreas.

65. The method of claim 57, wherein said cancer is cancer of the mouth, throat, pharynx, larynx, or esophagus,

66. The method of claim 57, further comprising using a 10q22 DNA probe.

67. A method for predicting the progression or metastasis of non-small cell carcinoma in a subject comprising:

(a) obtaining a lung test sample from a subject;
(b) providing a 10q22 DNA probe;
(c) contacting said probe with said test sample; and
(d) analyzing DNA from said test sample.

68. A method for the staging lung of cancer in a subject comprising determining the deletion distribution of a RPL 14, CD39L3, PMGM, or GC20 gene.

69. A method of determining likelihood of cancer relapse or development of a new primary cancer in a subject comprising determining genetic aberrations at chromosomal loci 3p21.3 or 10q22 in DNA of bronchial tissue adjacent to tumor tissue from said subject, wherein abnormalities in DNA of said adjacent tissue correlate with cancer relapse or development of said cancer.

70. The method of claim 69, wherein said cancer is lung cancer.

71. The method of claim 70, wherein said cancer is non-small cell carcinoma.

72. The method of claim 70, wherein said cancer is adenocarcinoma.

73. The method of claim 70, wherein said cancer is squamous cell carcinoma.

74. The method of claim 69, wherein said cancer is an upper airway primary or secondary cancer.

75. The method of claim 69, wherein said cancer is bladder cancer.

76. The method of claim 69, wherein said cancer is cancer of the head or neck.

77. The method of claim 69, wherein said cancer is urothelial.

78. The method of claim 69, wherein said cancer is cancer of the kidneys.

79. The method of claim 69, wherein said cancer is cancer of the pancreas.

80. The method of claim 69, wherein said cancer is cancer of the mouth, throat, pharynx, larynx, or esophagus.

81. The method of claim 69, wherein an RPL 14, CD39L3, PMGM, or GC20 gene probe is used.

82. The method of claim 69, wherein a 3p21.3 DNA probe is used.

83. The method of claim 69 wherein a 10q22 DNA probe is used.

84. The method of claim 82, further comprising use of a 10q22 DNA probe.

85. The method of claim 69, wherein said test sample comes from the same or contralateral lung.

86. The method of claim 69, wherein said test sample comes from nontumorous bronchial cells.

87. A method of identifying an individual to be segregated from a high risk environment comprising:

(a) obtaining a test sample from a subject;
(b) providing an RPL 14, CD39L3, PMGM, or GC20 gene probe
(c) contacting said probe with said test sample; and
(d) analyzing DNA from said test sample,

whereby said analysis is used to identify an individual who is highly susceptible to the development of lung cancer and who should not be exposed to a high risk environment.

88. The method of claim 87, further comprising providing a 10q22 or PTEN/MMAC1 gene probe.